

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 05:54:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124923.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR3124923 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124923_1.fastq.gz SRR3124923_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 05:54:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124923.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,623,998
Mapped reads	3,582,793 / 98.86%
Unmapped reads	41,205 / 1.14%
Mapped paired reads	3,582,793 / 98.86%
Mapped reads, first in pair	1,795,481 / 49.54%
Mapped reads, second in pair	1,787,312 / 49.32%
Mapped reads, both in pair	3,568,656 / 98.47%
Mapped reads, singletons	14,137 / 0.39%
Secondary alignments	0
Supplementary alignments	38,753 / 1.07%
Read min/max/mean length	30 / 151 / 151.52
Duplicated reads (estimated)	492,059 / 13.58%
Duplication rate	13.33%
Clipped reads	2,566,911 / 70.83%

2.2. ACGT Content

Number/percentage of A's	139,689,869 / 28.87%
Number/percentage of C's	99,687,446 / 20.6%
Number/percentage of T's	139,131,690 / 28.75%
Number/percentage of G's	105,403,537 / 21.78%
Number/percentage of N's	20,937 / 0%

GC Percentage	42.38%
---------------	--------

2.3. Coverage

Mean	0.1564
Standard Deviation	1.5785

2.4. Mapping Quality

Mean Mapping Quality	53.81
----------------------	-------

2.5. Insert size

Mean	66,865.56
Standard Deviation	2,451,935.76
P25/Median/P75	138 / 170 / 215

2.6. Mismatches and indels

General error rate	1.36%
Mismatches	6,423,298
Insertions	83,408
Mapped reads with at least one insertion	2.23%
Deletions	171,539
Mapped reads with at least one deletion	4.63%
Homopolymer indels	46.54%

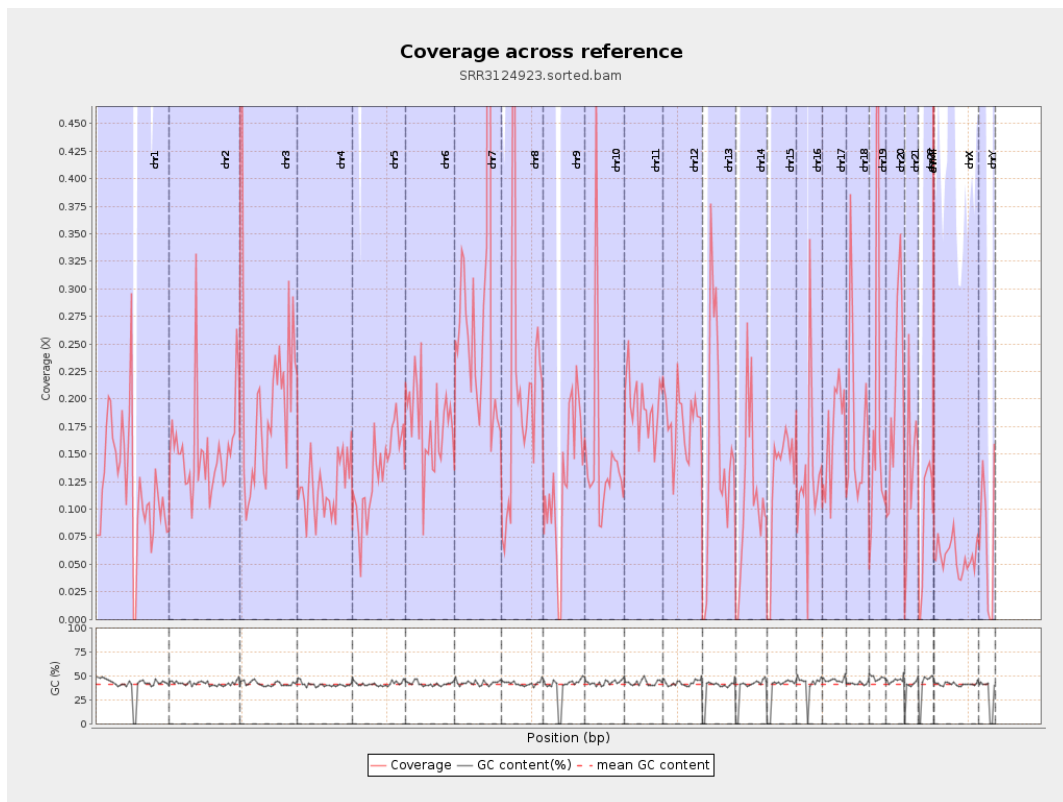
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
------	--------	--------	------	----------

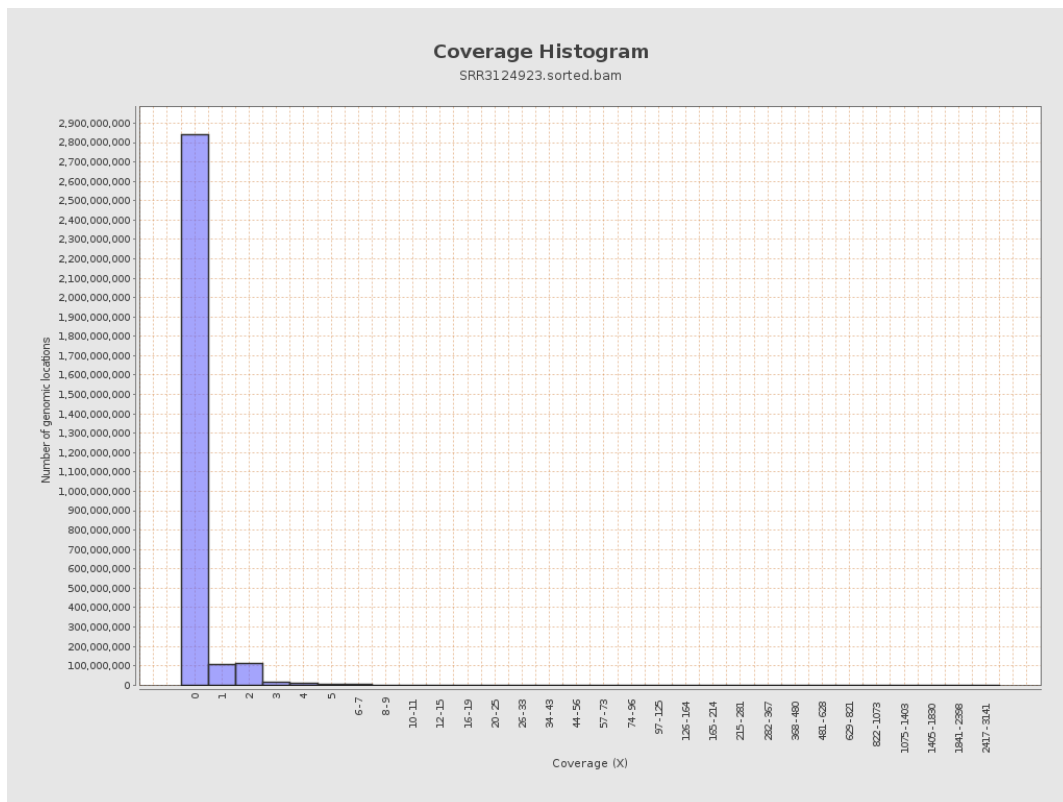
		bases	coverage	deviation
chr1	249250621	30217218	0.1212	2.8971
chr2	243199373	37407866	0.1538	1.497
chr3	198022430	40879704	0.2064	0.7287
chr4	191154276	22810521	0.1193	0.744
chr5	180915260	24145624	0.1335	0.5289
chr6	171115067	30377237	0.1775	1.1147
chr7	159138663	49710735	0.3124	2.6611
chr8	146364022	29418918	0.201	0.8561
chr9	141213431	18041919	0.1278	1.5811
chr10	135534747	19706891	0.1454	3.5914
chr11	135006516	26054062	0.193	1.0979
chr12	133851895	23921189	0.1787	0.6086
chr13	115169878	17335220	0.1505	0.5797
chr14	107349540	11889143	0.1108	0.5078
chr15	102531392	13222761	0.129	0.5274
chr16	90354753	11604929	0.1284	1.7252
chr17	81195210	13811834	0.1701	1.1762
chr18	78077248	14113238	0.1808	1.7515
chr19	59128983	12418938	0.21	1.6109
chr20	63025520	12930226	0.2052	0.7048
chr21	48129895	6553651	0.1362	0.6227
chr22	51304566	4590820	0.0895	0.43
chrMT	16571	20879	1.26	1.6769
chrX	155270560	8835009	0.0569	0.435

chrY	59373566	4233242	0.0713	1.2169
------	----------	---------	--------	--------

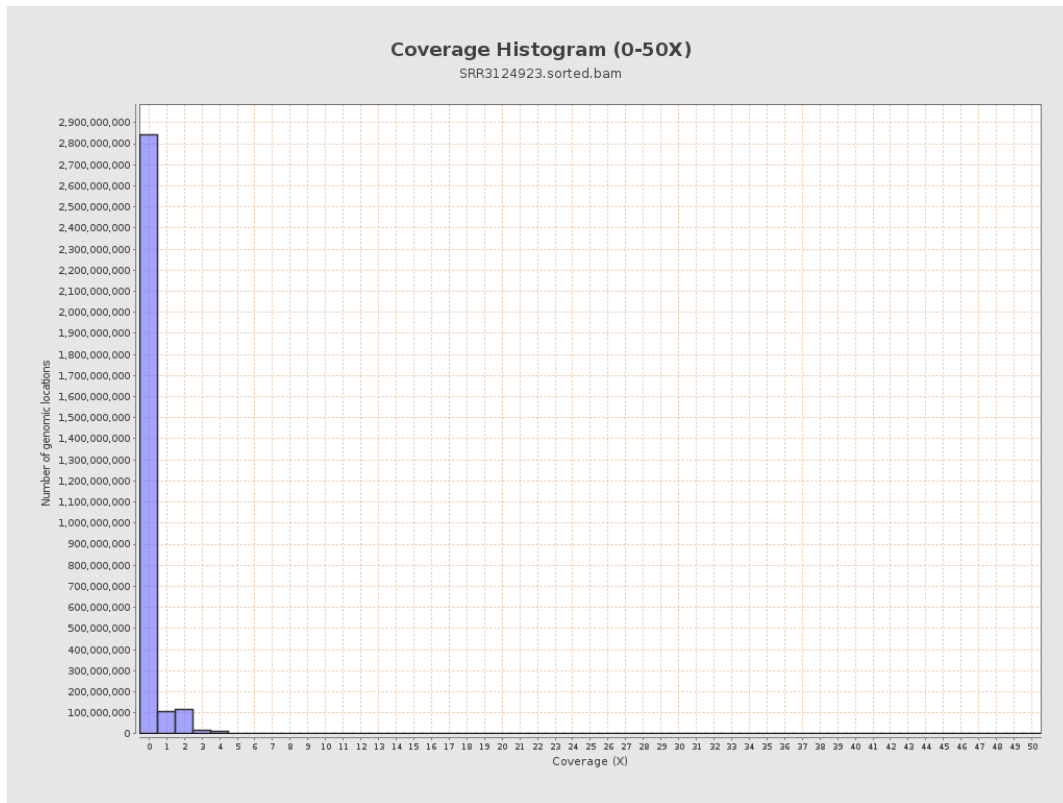
3. Results : Coverage across reference



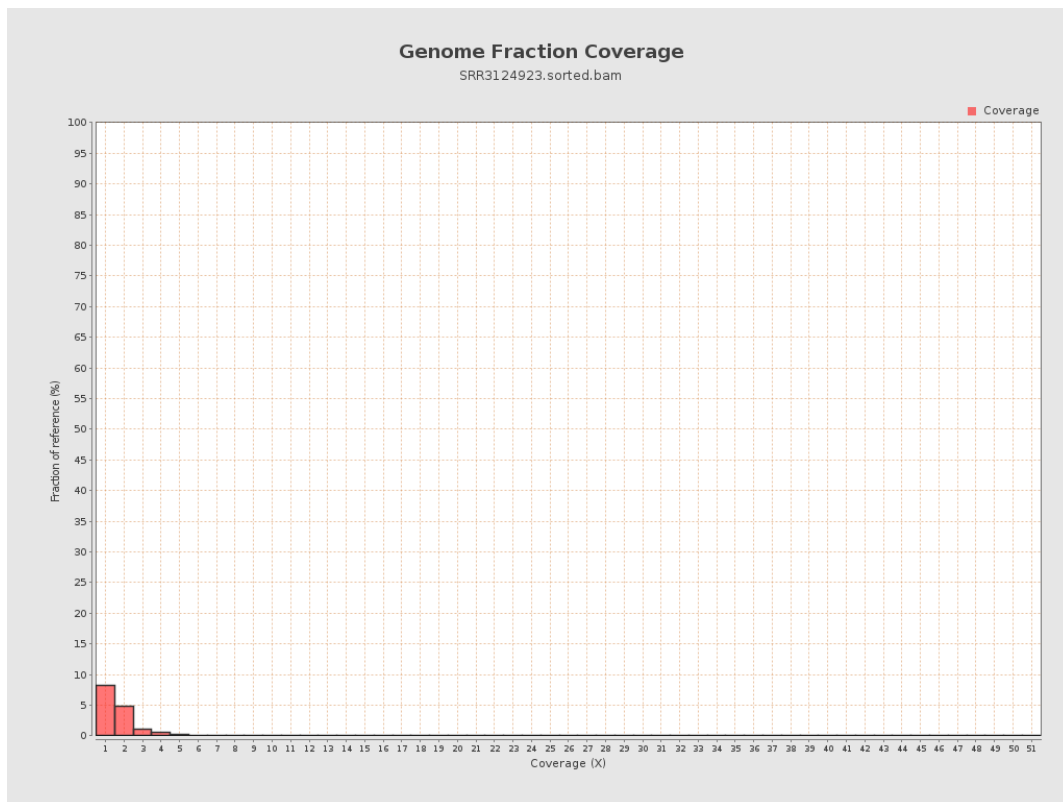
4. Results : Coverage Histogram



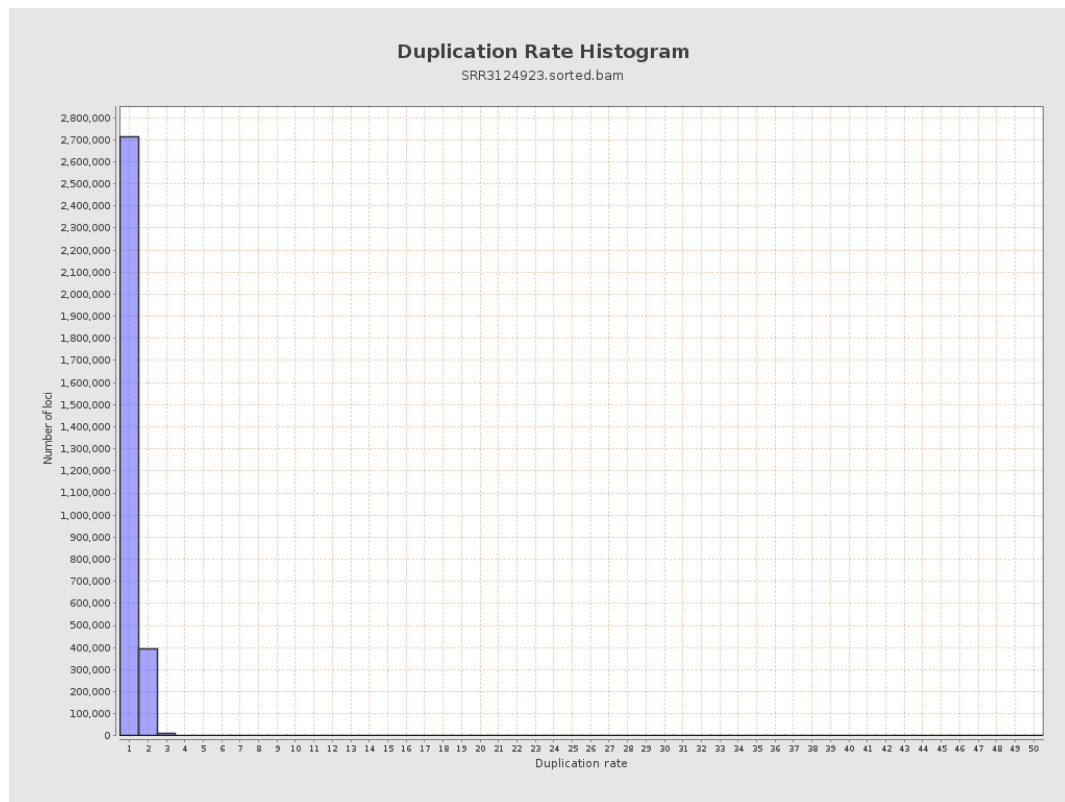
5. Results : Coverage Histogram (0-50X)



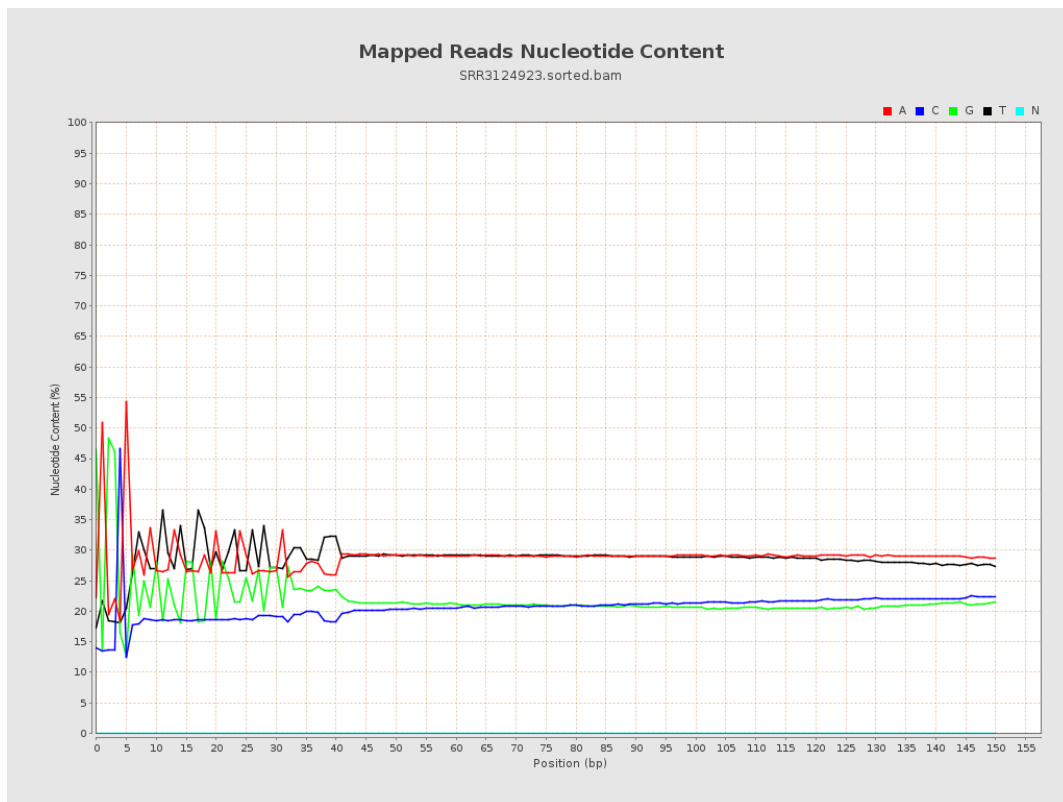
6. Results : Genome Fraction Coverage



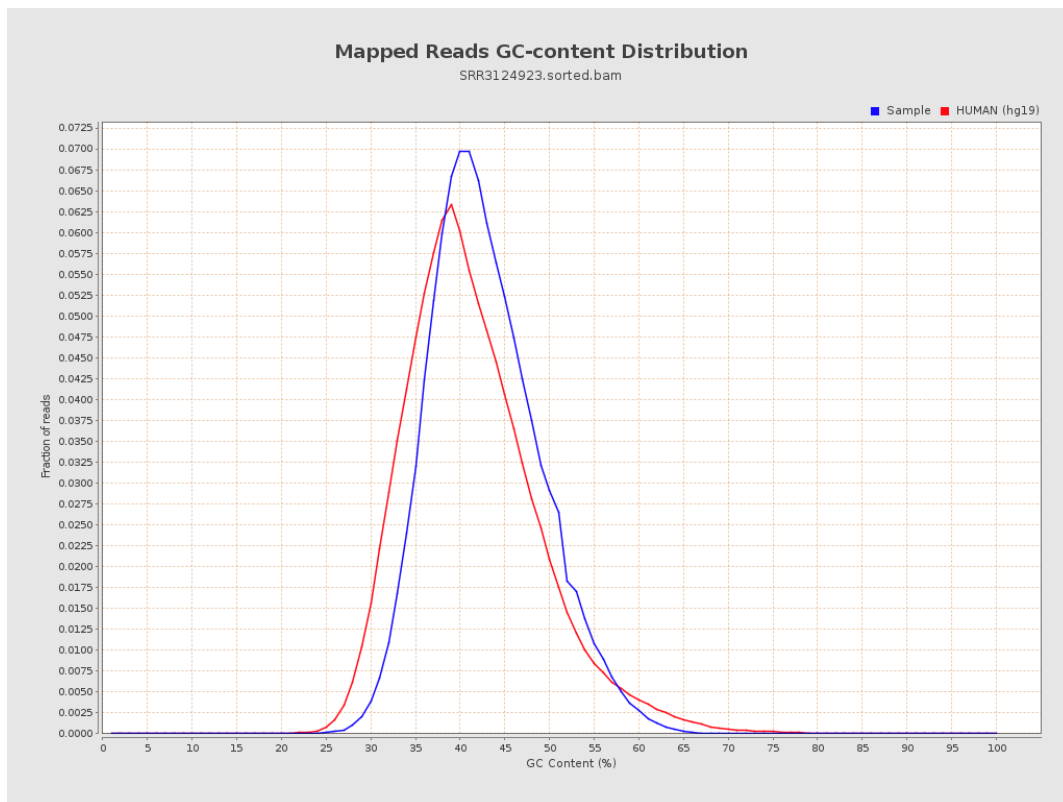
7. Results : Duplication Rate Histogram



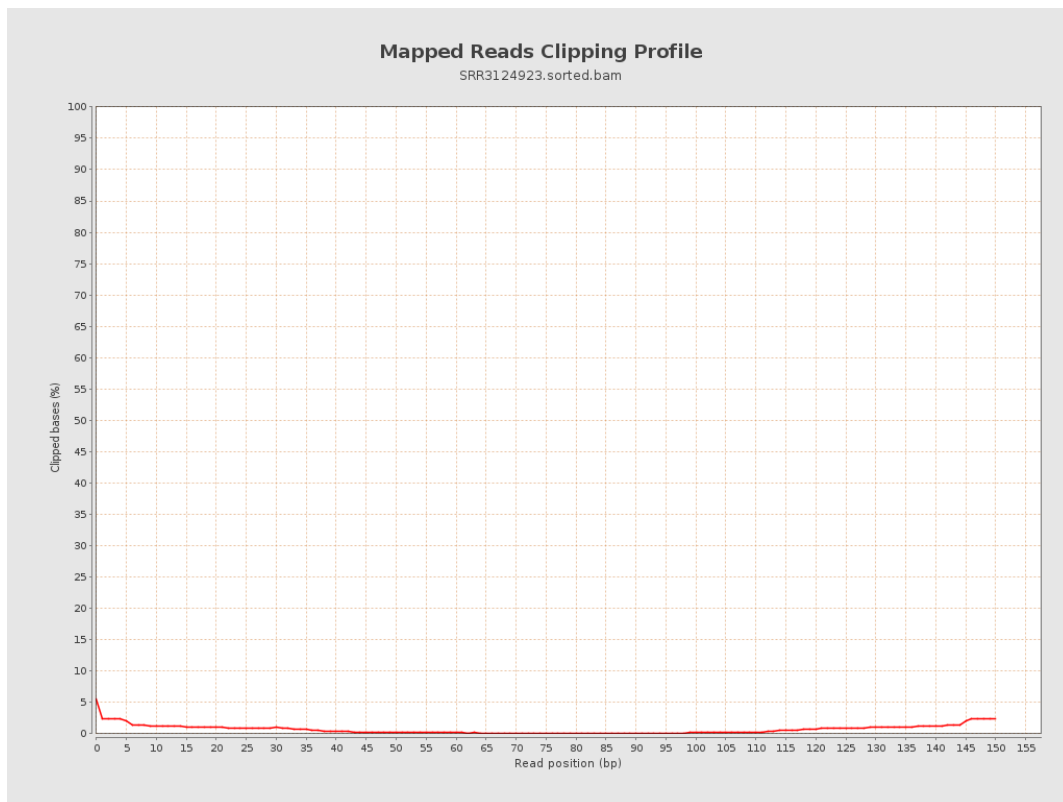
8. Results : Mapped Reads Nucleotide Content



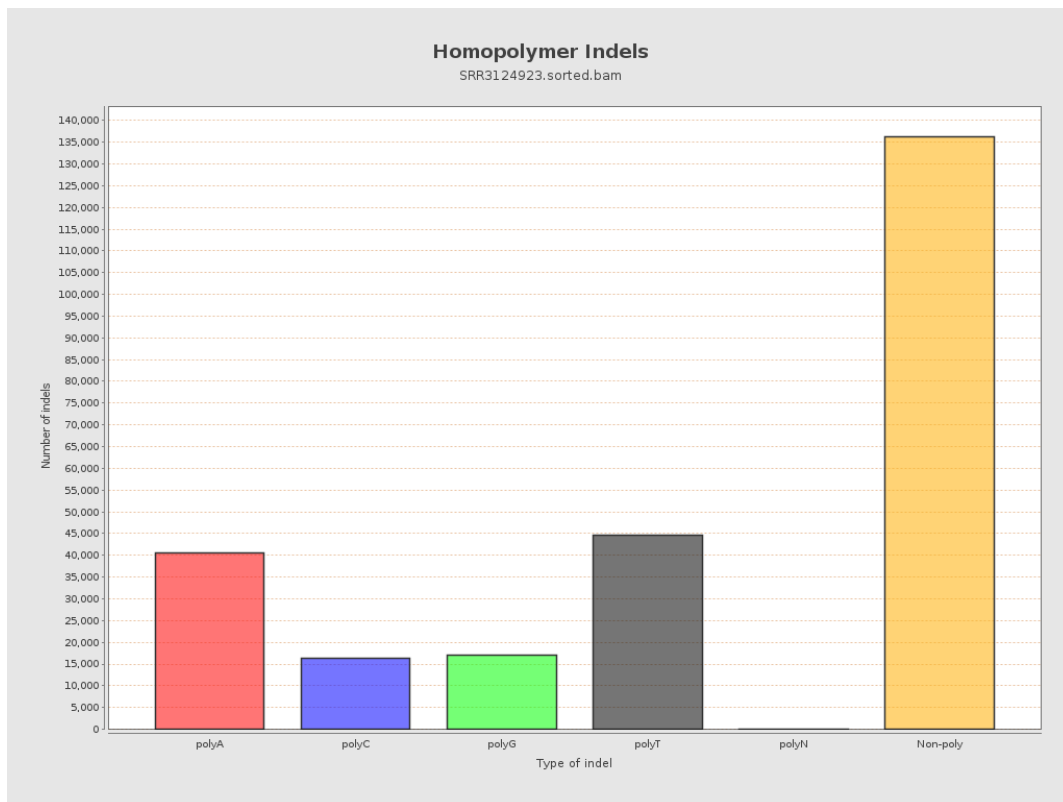
9. Results : Mapped Reads GC-content Distribution



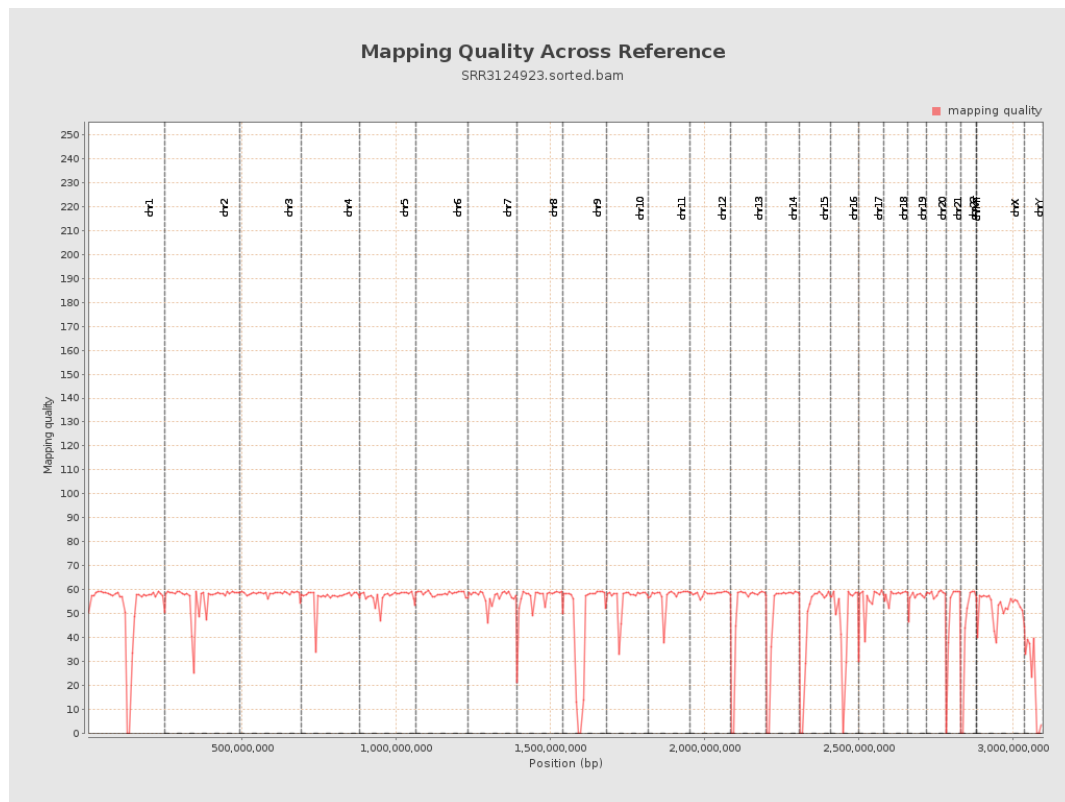
10. Results : Mapped Reads Clipping Profile



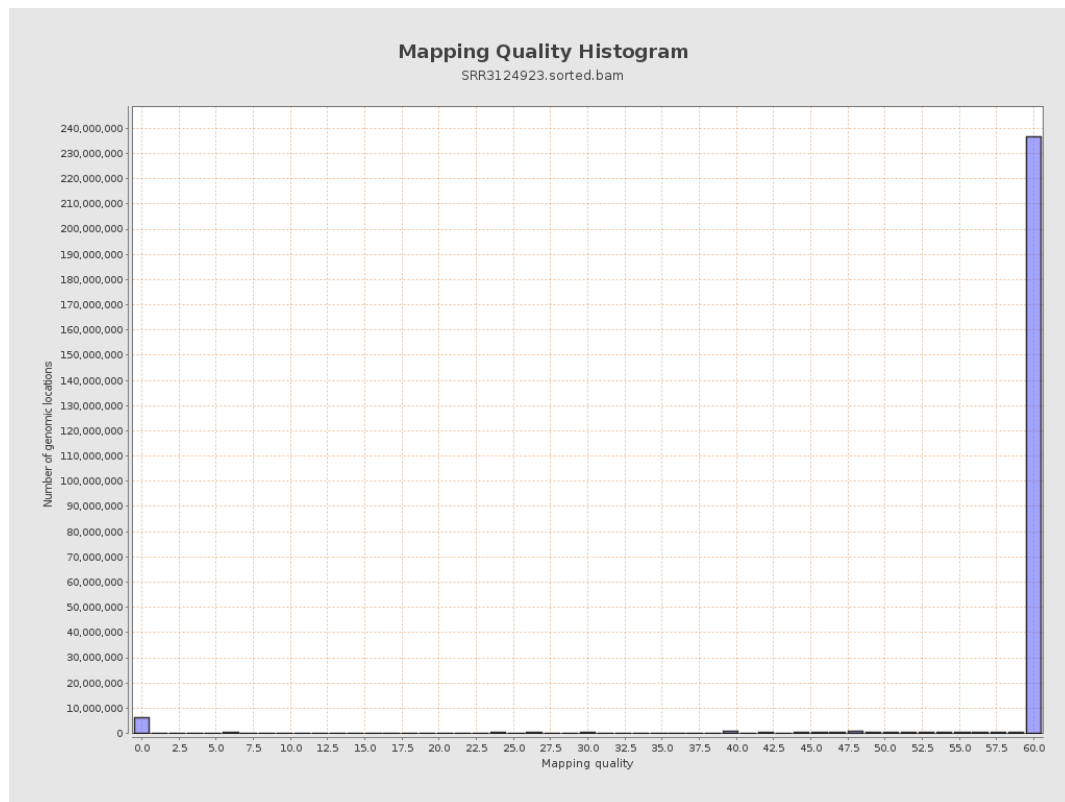
11. Results : Homopolymer Indels



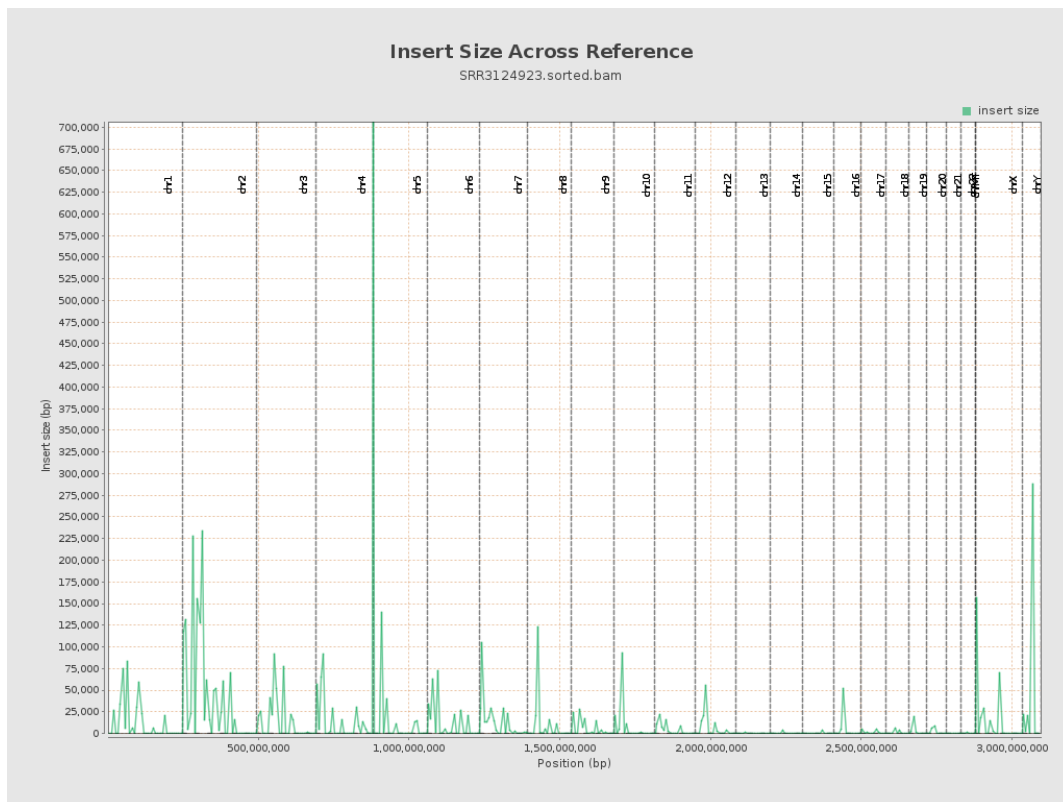
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

